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IN BRIEF

GENE EXPRESSION

Protein-mediated mRNA interference

The authors identified a protein in the archaeon *Haloquadratum walsbyi* that cleaves mRNAs at a specific 7-base sequence. This protein, MazF-hw, is a homologue of mRNA interferases identified in bacteria, but the previously identified proteins recognize shorter sequences. The longer sequence may achieve a similar level of mRNA regulation specificity to that conferred by microRNAs or by small interfering RNAs. Indeed, the MazF-hw target site is enriched in particular genes, including in a rhodopsin transcription activator. It is possible that highly specific mRNA interferases could be developed as tools to control gene expression.

ORIGINAL RESEARCH PAPER Yamaguchi, Y. *et al.* Inhibition of specific gene expressions by protein-mediated mRNA interference. *Nature Commun.* **3**, 607 (2012)

GENOMIC INSTABILITY

Transgenerational effects of anticancer drugs

Do chemotherapeutic drugs have effects on the offspring of treated individuals? These authors treated male mice with clinically relevant doses of one of three widely used anticancer drugs and then measured the mutation rate at an expanded simple tandem repeat in the bone marrow and germline of their offspring using single-molecule PCR. They found a significant increase in mutations in both tissues and, intriguingly, in the maternal allele as well as the allele from the exposed father. It will be interesting to study the molecular basis of the effect and whether similar influences are seen in humans.

ORIGINAL RESEARCH PAPER Glen, C. D. & Dubrova, Y. E. Exposure to anticancer drugs can result in transgenerational genomic instability in mice. *Proc. Natl Acad. Sci.* 30 Jan 2012 (doi:10.1073/pnas.1119396109)

CANCER

Genomic and epigenomic analyses of cancer

The February issue of *Genome Research* includes a range of papers describing the genomic and epigenomic profiling of various cancer types. The publications cover: the identification of genomic markers to be used in disease diagnosis and monitoring; the use of next-generation sequencing tools to characterize the cancer mutational landscape; a study of the interplay of DNA methylation and chromatin dynamics in cancer; and a description of computational resources for analysing sequence, pathway and network data. The issue also contains commentaries from leading researchers on the translational potential of the new findings.

ORIGINAL RESEARCH PAPERS Special issue on cancer genomics. *Genome Res.* **22** (2012) http://genome.cshlp.org/content/22/2.toc?etoc

GENOME EVOLUTION

Unexpected relationship between mutation rate and genome complexity

The hypothesis that genome size and complexity are inversely correlated with mutation rate has been challenged by a study of mitochondrial genomes in the *Silene* plant genus. Contrary to expectation, species that have experienced recently accelerated mutation rates have the largest genomes of all angiosperms, whereas the genomes of slower mutating species are smaller than average. The large genomes showed many structural alterations and changes in recombinational properties, suggesting that changes in mutation rate can drive rapid and unpredictable genome evolution.

ORIGINAL RESEARCH PAPER Sloan, D. B. *et al.* Rapid evolution of enormous, multichromosomal genomes in flowering plant mitochondria with exceptionally high mutation rates. *PLoS Biol.* **10**, e1001241 (2012)